

SEQUENCE LISTING

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1277 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10	ATG GTC GAA ATG CTG CTG TTG ACA AGA ATT CTC TTG GTG GGC TTC ATC	48
	Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile	
	1 5 10 15	
25	TGC GCT CTT TTA GTC TCC TCT GGG CTG ACT TGT GGA CCA GGC AGG GGC	96
	Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly	
	20 25 30	
30	ATT GGA AAA AGG AGG CAC CCC AAA AAG CTG ACC CCG TTA GCC TAT AAG	144
	Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys	
	35 40 45	
35	CAG TTT ATT CCC AAT GTG GCA GAG AAG ACC CTA GGG GCC AGT GGA AGA	192
	Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg	
	50 55 60	
40	TAT GAA GGG AAG ATC ACA AGA AAC TCC GAG AGA TTT AAA GAA CTA ACC	240
	Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr	
	65 70 75 80	
45	CCA AAT TAC AAC CCT GAC ATT ATT TTT AAG GAT GAA GAG AAC ACG GGA	288
	Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly	
	85 90 95	
50	GCT GAC AGA CTG ATG ACT CAG CGC TGC AAG GAC AAG CTG AAT GCC CTG	336
	Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu	
	100 105 110	
55	GCG ATC TCG GTG ATG AAC CAG TGG CCC GGG GTG AAG CTG CGG GTG ACC	384
	Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr	
	115 120 125	
60	GAG GGC TGG GAC GAG GAT GGC CAT CAC TCC GAG GAA TCG CTG CAC TAC	432
	Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr	
	130 135 140	
60	GAG GGT CGC GCC GTG GAC ATC ACC ACG TCG GAT CGG GAC CGC AGC AAG	480
	Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys	
	145 150 155 160	

	TAC	GGA	ATG	CTG	GCC	CGC	CTC	GCC	GTC	GAG	GCC	GGC	TTC	GAC	TGG	GTC	528
	Tyr	Gly	Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	
					165					170					175		
5	TAC	TAC	GAG	TCC	AAG	GCG	CAC	ATC	CAC	TGC	TCC	GTC	AAA	GCA	GAA	AAC	576
	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	
				180					185					190			
10	TCA	GTG	GCA	GCG	AAA	TCA	GGA	GGC	TGC	TTC	CCT	GGC	TCA	GCC	ACA	GTG	624
	Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	
			195					200					205				
15	CAC	CTG	GAG	CAT	GGA	GGC	ACC	AAG	CTG	GTG	AAG	GAC	CTG	AGC	CCT	GGG	672
	His	Leu	Glu	His	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Ser	Pro	Gly	
		210					215					220					
20	GAC	CGC	GTG	CTG	GCT	GCT	GAC	GCG	GAC	GGC	CGG	CTG	CTC	TAC	AGT	GAC	720
	Asp	Arg	Val	Leu	Ala	Ala	Asp	Ala	Asp	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	
	225				230						235					240	
25	TTC	CTC	ACC	TTC	CTC	GAC	CGG	ATG	GAC	AGC	TCC	CGA	AAG	CTC	TTC	TAC	768
	Phe	Leu	Thr	Phe	Leu	Asp	Arg	Met	Asp	Ser	Ser	Arg	Lys	Leu	Phe	Tyr	
				245						250					255		
30	GTC	ATC	GAG	ACG	CGG	CAG	CCC	CGG	GCC	CGG	CTG	CTA	CTG	ACG	GCG	GCC	816
	Val	Ile	Glu	Thr	Arg	Gln	Pro	Arg	Ala	Arg	Leu	Leu	Leu	Thr	Ala	Ala	
				260					265					270			
35	CAC	CTG	CTC	TTT	GTG	GCC	CCC	CAG	CAC	AAC	CAG	TCG	GAG	GCC	ACA	GGG	864
	His	Leu	Leu	Phe	Val	Ala	Pro	Gln	His	Asn	Gln	Ser	Glu	Ala	Thr	Gly	
			275				280						285				
40	TCC	ACC	AGT	GGC	CAG	GCG	CTC	TTC	GCC	AGC	AAC	GTG	AAG	CCT	GGC	CAA	912
	Ser	Thr	Ser	Gly	Gln	Ala	Leu	Phe	Ala	Ser	Asn	Val	Lys	Pro	Gly	Gln	
		290					295					300					
45	CGT	GTC	TAT	GTG	CTG	GGC	GAG	GGC	GGG	CAG	CAG	CTG	CTG	CCG	GCG	TCT	960
	Arg	Val	Tyr	Val	Leu	Gly	Glu	Gly	Gly	Gln	Gln	Leu	Leu	Pro	Ala	Ser	
	305				310					315						320	
50	GTC	CAC	AGC	GTC	TCA	TTG	CGG	GAG	GAG	GCG	TCC	GGA	GCC	TAC	GCC	CCA	1008
	Val	His	Ser	Val	Ser	Leu	Arg	Glu	Glu	Ala	Ser	Gly	Ala	Tyr	Ala	Pro	
				325						330					335		
55	CTC	ACC	GCC	CAG	GGC	ACC	ATC	CTC	ATC	AAC	CGG	GTG	TTG	GCC	TCC	TGC	1056
	Leu	Thr	Ala	Gln	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	
			340						345					350			
60	TAC	GCC	GTC	ATC	GAG	GAG	CAC	AGT	TGG	GCC	CAT	TGG	GCC	TTC	GCA	CCA	1104
	Tyr	Ala	Val	Ile	Glu	Glu	His	Ser	Trp	Ala	His	Trp	Ala	Phe	Ala	Pro	
			355					360					365				
65	TTC	CGC	TTG	GCT	CAG	GGG	CTG	CTG	GCC	GCC	CTC	TGC	CCA	GAT	GGG	GCC	1152
	Phe	Arg	Leu	Ala	Gln	Gly	Leu	Leu	Ala	Ala	Leu	Cys	Pro	Asp	Gly	Ala	
		370					375					380					
70	ATC	CCT	ACT	GCC	GCC	ACC	ACC	ACC	ACT	GGC	ATC	CAT	TGG	TAC	TCA	CGG	1200
	Ile	Pro	Thr	Ala	Ala	Thr	Thr	Thr	Thr	Gly	Ile	His	Trp	Tyr	Ser	Arg	
	385					390					395					400	

CTC CTC TAC CGC ATC GGC AGC TGG GTG CTG GAT GGT GAC GCG CTG CAT 1248
 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
 405 410 415

5 CCG CTG GGC ATG GTG GCA CCG GCC AGC TG 1277
 Pro Leu Gly Met Val Ala Pro Ala Ser
 420 425

10 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 1190 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..1191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

30 ATG GCT CTG CCG GCC AGT CTG TTG CCC CTG TGC TGC TTG GCA CTC TTG 48
 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
 1 5 10 15

35 GCA CTA TCT GCC CAG AGC TGC GGG CCG GGC CGA GGA CCG GTT GGC CGG 96
 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
 20 25 30

40 CGG CGT TAT GTG CGC AAG CAA CTT GTG CCT CTG CTA TAC AAG CAG TTT 144
 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
 35 40 45

GTG CCC AGT ATG CCC GAG CGG ACC CTG GGC GCG AGT GGG CCA GCG GAG 192
 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
 50 55 60

45 GGG AGG GTA ACA AGG GGG TCG GAG CGC TTC CCG GAC CTC GTA CCC AAC 240
 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
 65 70 75 80

50 TAC AAC CCC GAC ATA ATC TTC AAG GAT GAG GAG AAC AGC GGC GCA GAC 288
 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
 85 90 95

55 CGC CTG ATG ACA GAG CGT TGC AAA GAG CGG GTG AAC GCT CTA GCC ATC 336
 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
 100 105 110

60 GCG GTG ATG AAC ATG TGG CCC GGA GTA CGC CTA CGT GTG ACT GAA GGC 384
 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125

	TGG	GAC	GAG	GAC	GGC	CAC	CAC	GCA	CAG	GAT	TCA	CTC	CAC	TAC	GAA	GGC	432
	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly	
	130							135							140		
5	CGT	GCC	TTG	GAC	ATC	ACC	ACG	TCT	GAC	CGT	GAC	CGT	AAT	AAG	TAT	GGT	480
	Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly	
	145					150					155					160	
10	TTG	TTG	GCG	CGC	CTA	GCT	GTG	GAA	GCC	GGA	TTC	GAC	TGG	GTC	TAC	TAC	528
	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
					165					170					175		
15	GAG	TCC	CGC	AAC	CAC	ATC	CAC	GTA	TCG	GTC	AAA	GCT	GAT	AAC	TCA	CTG	576
	Glu	Ser	Arg	Asn	His	Ile	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu	
				180					185					190			
20	GCG	GTC	CGA	GCC	GGA	GGC	TGC	TTT	CCG	GGA	AAT	GCC	ACG	GTG	CGC	TTG	624
	Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu	
				195				200					205				
25	CGG	AGC	GGC	GAA	CGG	AAG	GGG	CTG	AGG	GAA	CTA	CAT	CGT	GGT	GAC	TGG	672
	Arg	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp	
		210					215					220					
30	GTA	CTG	GCC	GCT	GAT	GCA	GCG	GCC	CGA	GTG	GTA	CCC	ACG	CCA	GTG	CTG	720
	Val	Leu	Ala	Ala	Asp	Ala	Ala	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu	
		225				230					235					240	
35	CTC	TTC	CTG	GAC	CGG	GAT	CTG	CAG	GGC	CGC	GCC	TCG	TTC	GTG	GCT	GTG	768
	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val	
					245				250						255		
40	GAG	ACC	GAG	CGG	CCT	CCG	CGC	AAA	CTG	TTG	CTC	ACA	CCC	TGG	CAT	CTG	816
	Glu	Thr	Glu	Arg	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu	
				260					265					270			
45	GTG	TTC	GCT	GCT	CGC	GGG	CCA	GCG	CCT	GCT	CCA	GGT	GAC	TTT	GCA	CCG	864
	Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro	
				275				280					285				
50	GTG	TTC	GCG	CGC	CGC	TTA	CGT	GCT	GGC	GAC	TCG	GTG	CTG	GCT	CCC	GGC	912
	Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly	
				290			295					300					
55	GGG	GAC	GCG	CTC	CAG	CCG	GCG	CGC	GTA	GCC	CGC	GTG	GCG	CGC	GAG	GAA	960
	Gly	Asp	Ala	Leu	Gln	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu	
		305				310					315					320	
60	GCC	GTG	GGC	GTG	TTC	GCA	CCG	CTC	ACT	GCG	CAC	GGG	ACG	CTG	CTG	GTC	1008</

1152

1190

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1281 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) **FEATURE:**

(A) NAME/KEY: CDS

(B) LOCATION: 1..1233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

48

96

144

192

240

288

336

384

432

	Val	Thr	Glu	Gly	Arg	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	
	130						135					140					
5	CAC	TAT	GAG	GGC	CGC	GCG	GTG	GAT	ATC	ACC	ACC	TCA	GAC	CGT	GAC	CGA	480
	His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	
	145					150					155					160	
10	AAT	AAG	TAT	GGA	CTG	CTG	GCG	CGC	TTA	GCA	GTG	GAG	GCC	GGC	TTC	GAC	528
	Asn	Lys	Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	
					165					170					175		
15	TGG	GTG	TAT	TAC	GAG	TCC	AAG	GCC	CAC	GTG	CAT	TGC	TCT	GTC	AAG	TCT	576
	Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser	
				180					185					190			
20	GAG	CAT	TCG	GCC	GCT	GCC	AAG	ACA	GGT	GGC	TGC	TTT	CCT	GCC	GGA	GCC	624
	Glu	His	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	
			195				200						205				
25	CAG	GTG	CGC	CTA	GAG	AAC	GGG	GAG	CGT	GTG	GCC	CTG	TCA	GCT	GTA	AAG	672
	Gln	Val	Arg	Leu	Glu	Asn	Gly	Glu	Arg	Val	Ala	Leu	Ser	Ala	Val	Lys	
		210					215					220					
30	CCA	GGA	GAC	CGG	GTG	CTG	GCC	ATG	GGG	GAG	GAT	GGG	ACC	CCC	ACC	TTC	720
	Pro	Gly	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Thr	Pro	Thr	Phe	
		225				230					235					240	
35	AGT	GAT	GTG	CTT	ATT	TTC	CTG	GAC	CGC	GAG	CCA	AAC	CGG	CTG	AGA	GCT	768
	Ser	Asp	Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	Asn	Arg	Leu	Arg	Ala	
					245				250						255		
40	TTC	CAG	GTC	ATC	GAG	ACT	CAG	GAT	CCT	CCG	CGT	CGG	CTG	GCG	CTC	ACG	816
	Phe	Gln	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	
				260					265					270			
45	CCT	GCC	CAC	CTG	CTC	TTC	ATT	GCG	GAC	AAT	CAT	ACA	GAA	CCA	GCA	GCC	864
	Pro	Ala	His	Leu	Leu	Phe	Ile	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala	
			275					280					285				
50	CAC	TTC	CGG	GCC	ACA	TTT	GCC	AGC	CAT	GTG	CAA	CCA	GGC	CAA	TAT	GTG	912
	His	Phe	Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val	
		290					295					300					
55	CTG	GTA	TCA	GGG	GTA	CCA	GGC	CTC	CAG	CCT	GCT	CGG	GTG	GCA	GCT	GTC	960
	Leu	Val	Ser	Gly	Val	Pro	Gly	Leu	Gln	Pro	Ala	Arg	Val	Ala	Ala	Val	
		305				310					315					320	
60	TCC	ACC	CAC	GTG	GCC	CTT	GGG	TCC	TAT	GCT	CCT	CTC	ACA	AGG	CAT	GGG	1008
	Ser	Thr	His	Val	Ala	Leu	Gly	Ser	Tyr	Ala	Pro	Leu	Thr	Arg	His	Gly	
					325					330					335		
65	ACA	CTT	GTG	GTG	GAG	GAT	GTG	GTG	GCC	TCC	TGC	TTT	GCA	GCT	GTG	GCT	1056
	Thr	Leu	Val	Val	Glu	Asp	Val	Val	Ala	Ser	Cys	Phe	Ala	Ala	Val	Ala	
				340					345				350				
70	GAC	CAC	CAT	CTG	GCT	CAG	TTG	GCC	TTC	TGG	CCC	CTG	CGA	CTG	TTT	CCC	1104
	Asp	His	His	Leu	Ala	Gln	Leu	Ala	Phe	Trp	Pro	Leu	Arg	Leu	Phe	Pro	
			355					360					365				
75	AGT	TTG	GCA	TGG	GGC	AGC	TGG	ACC	CCA	AGT	GAG	GGT	GTT	CAC	TCC	TAC	1152

662030 203520

CGG CTG ATG ACT CAG AGG TGC AAA GAC AAG TTA AAT GGC TTG GCC ATC 336
Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile
100 105 110

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

	TCT	GTG	ATG	AAC	CAG	TGG	CCT	GGA	GTG	AGG	CTG	CGA	GTG	ACC	GAG	GGC	384
	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	
			115					120					125				
5	TGG	GAT	GAG	GAC	GGC	CAT	CAT	TCA	GAG	GAG	TCT	CTA	CAC	TAT	GAG	GGT	432
	Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	
		130					135					140					
10	CGA	GCA	GTG	GAC	ATC	ACC	ACG	TCC	GAC	CGG	GAC	CGC	AGC	AAG	TAC	GGC	480
	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	Tyr	Gly	
		145				150					155					160	
	ATG	CTG	GCT	CGC	CTG	GCT	GTG	GAA	GCA	GGT	TTC	GAC	TGG	GTC	TAC	TAT	528
15	Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
					165					170					175		
	GAA	TCC	AAA	GCT	CAC	ATC	CAC	TGT	TCT	GTG	AAA	GCA	GAG	AAC	TCC	GTG	576
	Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	
				180				185						190			
20	GCG	GCC	AAA	TCC	GGC	GGC	TGT	TTC	CCG	GGA	TCC	GCC	ACC	GTG	CAC	CTG	624
	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	His	Leu	
			195					200					205				
25	GAG	CAG	GGC	GGC	ACC	AAG	CTG	GTG	AAG	GAC	TTA	CGT	CCC	GGA	GAC	CGC	672
	Glu	Gln	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Arg	
		210					215					220					
30	GTG	CTG	GCG	GCT	GAC	GAC	CAG	GGC	CGG	CTG	CTG	TAC	AGC	GAC	TTC	CTC	720
	Val	Leu	Ala	Ala	Asp	Asp	Gln	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	Phe	Leu	
		225				230					235					240	
	ACC	TTC	CTG	GAC	CGC	GAC	GAA	GGC	GCC	AAG	AAG	GTC	TTC	TAC	GTG	ATC	768
35	Thr	Phe	Leu	Asp	Arg	Asp	Glu	Gly	Ala	Lys	Lys	Val	Phe	Tyr	Val	Ile	
					245					250					255		
	GAG	ACG	CTG	GAG	CCG	CGC	GAG	CGC	CTG	CTG	CTC	ACC	GCC	GCG	CAC	CTG	816
	Glu	Thr	Leu	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu	
				260				265						270			
40	CTC	TTC	GTG	GCG	CCG	CAC	AAC	GAC	TCG	GGG	CCC	ACG	CCC	GGG	CCA	AGC	864
	Leu	Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Gly	Pro	Thr	Pro	Gly	Pro	Ser	
			275					280					285				
45	GCG	CTC	TTT	GCC	AGC	CGC	GTG	CGC	CCC	GGG	GAG	CGC	GTG	TAC	GTG	GTG	912
	Ala	Leu	Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val	
		290					295					300					
50	GCT	GAA	CGC	GGC	GGG	GAC	CGC	CGG	CTG	CTG	CCC	GCC	GCG	GTG	CAC	AGC	960
	Ala	Glu	Arg														

5 ATC GAG GAG CAC AGC TGG GCA CAC CGG GCC TTC GCG CCT TTC CGC CTG 1104
 Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu
 355 360 365

10 GCG CAC GCG CTG CTG GCC GCG CTG GCA CCC GCC CGC ACG GAC GGC GGG 1152
 Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly
 370 375 380

15 GGC GGG GGC AGC ATC CCT GCA GCG CAA TCT GCA ACG GAA GCG AGG GGC 1200
 Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly
 385 390 395 400

20 GCG GAG CCG ACT GCG GGC ATC CAC TGG TAC TCG CAG CTG CTC TAC CAC 1248
 Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His
 405 410 415

25 ATT GGC ACC TGG CTG TTG GAC AGC GAG ACC ATG CAT CCC TTG GGA ATG 1296
 Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met
 420 425 430

30 GCG GTC AAG TCC AGC TG 1313
 Ala Val Lys Ser Ser
 435

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

45 ATG CGG CTT TTG ACG AGA GTG CTG CTG GTG TCT CTT CTC ACT CTG TCC 48
 Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser
 1 5 10 15

50 TTG GTG GTG TCC GGA CTG GCC TGC GGT CCT GGC AGA GGC TAC GGC AGA 96
 Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg
 20 25 30

55 AGA AGA CAT CCG AAG AAG CTG ACA CCT CTC GGC TAC AAG CAG TTC ATA 144
 Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
 35 40 45

60 CCT AAT GTC GCG GAG AAG ACC TTA GGG GCC AGC GGC AGA TAC GAG GGC 192
 Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
 50 55 60

60 AAG ATA ACG CGC AAT TCG GAG AGA TTT AAA GAA CTT ACT CCA AAT TAC 240

	Lys 65	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	
						70					75					80	
5	AAT Asn	CCC Pro	GAC Asp	ATT Ile	ATC Ile	TTT Phe	AAG Lys	GAT Asp	GAG Glu	GAG Glu	AAC Asn	ACG Thr	GGA Gly	GCG Ala	GAC Asp	AGG Arg	288
				85						90					95		
10	CTC Leu	ATG Met	ACA Thr	CAG Gln	AGA Arg	TGC Cys	AAA Lys	GAC Asp	AAG Lys	CTG Leu	AAC Asn	TCG Ser	CTG Leu	GCC Ala	ATC Ile	TCT Ser	336
				100					105					110			
15	GTA Val	ATG Met	AAC Asn	CAC His	TGG Trp	CCA Pro	GGG Gly	GTT Val	AAG Lys	CTG Leu	CGT Arg	GTG Val	ACA Thr	GAG Glu	GGC Gly	TGG Trp	384
			115					120					125				
20	GAT Asp	GAG Glu	GAC Asp	GGT Gly	CAC His	CAT His	TTT Phe	GAA Glu	GAA Glu	TCA Ser	CTC Leu	CAC His	TAC Tyr	GAG Glu	GGA Gly	AGA Arg	432
			130				135					140					
25	GCT Ala	GTT Val	GAT Asp	ATT Ile	ACC Thr	ACC Thr	TCT Ser	GAC Asp	CGA Arg	GAC Asp	AAG Lys	AGC Ser	AAA Lys	TAC Tyr	GGG Gly	ACA Thr	480
						150					155					160	
30	CTG Leu	TCT Ser	CGC Arg	CTA Leu	GCT Ala	GTG Val	GAG Glu	GCT Ala	GGA Gly	TTT Phe	GAC Asp	TGG Trp	GTC Val	TAT Tyr	TAC Tyr	GAG Glu	528
					165					170					175		
35	TCC Ser	AAA Lys	GCC Ala	CAC His	ATT Ile	CAT His	TGC Cys	TCT Ser	GTC Val	AAA Lys	GCA Ala	GAA Glu	AAT Asn	TCG Ser	GTT Val	GCT Ala	576
				180					185					190			
40	GCG Ala	AAA Lys	TCT Ser	GGG Gly	GGC Gly	TGT Cys	TTC Phe	CCA Pro	GGT Gly	TCG Ser	GCT Ala	CTG Leu	GTC Val	TCG Ser	CTC Leu	CAG Gln	624
			195					200					205				
45	GAC Asp	GGA Gly	GGA Gly	CAG Gln	AAG Lys	GCC Ala	GTG Val	AAG Lys	GAC Asp	CTG Leu	AAC Asn	CCC Pro	GGA Gly	GAC Asp	AAG Lys	GTG Val	672
			210				215					220					
50	CTG Leu	GCG Ala	GCA Ala	GAC Asp	AGC Ser	GCG Ala	GGA Gly	AAC Asn	CTG Leu	GTG Val	TTC Phe	AGC Ser	GAC Asp	TTC Phe	ATC Ile	ATG Met	720
						230					235					240	
55	TTC Phe	ACA Thr	GAC Asp	CGA Arg	GAC Asp	TCC Ser	ACG Thr	ACG Thr	CGA Arg	CGT Arg	GTG Val	TTT Phe	TAC Tyr	GTC Val	ATA Ile	GAA Glu	768
					245					250					255		
60	ACG Thr	CAA Gln	GAA Glu	CCC Pro	GTT Val	GAA Glu	AAG Lys	ATC Ile	ACC Thr	CTC Leu	ACC Thr	GCC Ala	GCT Ala	CAC His	CTC Leu	CTT Leu	816
				260					265					270			
65	TTT Phe	GTC Val	CTC Leu	GAC Asp	AAC Asn	TCA Ser	ACG Thr	GAA Glu	GAT Asp	CTC Leu	CAC His	AGC Thr	ATG Met	ACC Thr	GCC Ala	GCG Ala	864
			275					280					285				
70	TAT Tyr	GCC Ala	AGC Ser	AGT Ser	GTC Val	AGA Arg	GCC Ala	GGA Gly	CAA Gln	AAG Lys	GTG Val	ATG Met	GTT Val	GTT Val	GAT Asp	GAT Asp	912
			290				295					300					
75	AGC	GGT	CAG	CTT	AAA	TCT	GTC	ATC	GTG	CAG	CGG	ATA	TAC	ACG			

Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu
 305 310 315 320

5 CAG CGG GGC TCG TTC GCA CCA GTG ACT GCA CAT GGG ACC ATT GTG GTC 1008
 Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val
 325 330 335

10 GAC AGA ATA CTG GCG TCC TGT TAC GCC GTA ATA GAG GAC CAG GGG CTT 1056
 Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu
 340 345 350

15 GCG CAT TTG GCC TTC GCG CCC GCC AGG CTC TAT TAT TAC GTG TCA TCA 1104
 Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser
 355 360 365

20 TTC CTG TCC CCC AAA ACT CCA GCA GTC GGT CCA ATG CGA CTT TAC AAC 1152
 Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn
 370 375 380

25 AGG AGG GGG TCC ACT GGT ACT CCA GGC TCC TGT CAT CAA ATG GGA ACG 1200
 Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr
 385 390 395 400

30 TGG CTT TTG GAC AGC AAC ATG CTT CAT CCT TTG GGG ATG TCA GTA AAC 1248
 Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn
 405 410 415

TCA AGC TG 1256
 Ser Ser

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

50 ATG CTG CTG CTG GCG AGA TGT CTG CTG CTA GTC CTC GTC TCC TCG CTG 48
 Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu
 1 5 10 15

55 CTG GTA TGC TCG GGA CTG GCG TGC GGA CCG GGC AGG GGG TTC GGG AAG 96
 Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys
 20 25 30

60 AGG AGG CAC CCC AAA AAG CTG ACC CCT TTA GCC TAC AAG CAG TTT ATC 144
 Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile

66030"2093260

	35					40					45						
5	CCC Pro	AAT Asn	GTG Val	GCC Ala	GAG Glu	AAG Lys	ACC Thr	CTA Leu	GGC Gly	GCC Ala	AGC Ser	GGA Gly	AGG Arg	TAT Tyr	GAA Glu	GGG Gly	192
	50					55					60						
10	AAG Lys	ATC Ile	TCC Ser	AGA Arg	AAC Asn	TCC Ser	GAG Glu	CGA Arg	TTT Phe	AAG Lys	GAA Glu	CTC Leu	ACC Thr	CCC Pro	AAT Asn	TAC Tyr	240
	65					70				75						80	
15	AAC Asn	CCC Pro	GAC Asp	ATC Ile	ATA Ile	TTT Phe	AAG Lys	GAT Asp	GAA Glu	GAA Glu	AAC Asn	ACC Thr	GGA Gly	GCG Ala	GAC Asp	AGG Arg	288
					85				90						95		
20	CTG Leu	ATG Met	ACT Thr	CAG Gln	AGG Arg	TGT Cys	AAG Lys	GAC Asp	AAG Lys	TTG Leu	AAC Asn	GCT Ala	TTG Leu	GCC Ala	ATC Ile	TCG Ser	336
				100					105					110			
25	GTG Val	ATG Met	AAC Asn	CAG Gln	TGG Trp	CCA Pro	GGA Gly	GTG Val	AAA Lys	CTG Leu	CGG Arg	GTG Val	ACC Thr	GAG Glu	GGC Gly	TGG Trp	384
			115				120						125				
30	GAC Asp	GAA Glu	GAT Asp	GGC Gly	CAC His	CAC His	TCA Ser	GAG Glu	GAG Glu	TCT Ser	CTG Leu	CAC His	TAC Tyr	GAG Glu	GGC Gly	CGC Arg	432
		130					135					140					
35	GCA Ala	GTG Val	GAC Asp	ATC Ile	ACC Thr	ACG Thr	TCT Ser	GAC Asp	CGC Arg	GAC Asp	CGC Arg	AGC Ser	AAG Lys	TAC Tyr	GGC Gly	ATG Met	480
	145					150			155							160	
40	CTG Leu	GCC Ala	CGC Arg	CTG Leu	GCG Ala	GTG Val	GAG Glu	GCC Ala	GGC Gly	TTC Phe	GAC Asp	TGG Trp	GTG Val	TAC Tyr	TAC Tyr	GAG Glu	528
				165					170						175		
45	TCC Ser	AAG Lys	GCA Ala	CAT His	ATC Ile	CAC His	TGC Cys	TCG Ser	GTG Val	AAA Lys	GCA Ala	GAG Glu	AAC Asn	TCG Ser	GTG Val	GCG Ala	576
				180					185					190			
50	GCC Ala	AAA Lys	TCG Ser	GGA Gly	GGC Gly	TGC Cys	TTC Phe	CCG Pro	GGC Gly	TCG Ser	GCC Ala	ACG Thr	GTG Val	CAC His	CTG Leu	GAG Glu	624
		195						200					205				
55	CAG Gln	GGC Gly	GGC Gly	ACC Thr	AAG Lys	CTG Leu	GTG Val	AAG Lys	GAC Asp	CTG Leu	AGC Ser	CCC Pro	GGG Gly	GAC Asp	CGC Arg	GTG Val	672
	210					215						220					
60	CTG Leu	GCG Ala	GCG Ala	GAC Asp	GAC Asp	CAG Gln	GGC Gly	CGG Arg	CTG Leu	CTC Leu	TAC Tyr	AGC Ser	GAC Asp	TTC Phe	CTC Leu	ACT Thr	720
	225					230					235					240	
65	TTC Phe	CTG Leu	GAC Asp	CGC Arg	GAC Asp	GAC Asp	GGC Gly	GCC Ala	AAG Lys	AAG Lys	GTC Val	TTC Phe	TAC Tyr	GTG Val	ATC Ile	GAG Glu	768
				245					250						255		
70	ACG Thr	CGG Arg	GAG Glu	CCG Pro	CGC Arg	GAG Glu	CGC Arg	CTG Leu	CTG Leu	CTC Leu	ACC Thr	GCC Ala	GCG Ala	CAC His	CTG Leu	CTC Leu	816
				260				265						270			
75	TTT Phe	GTG Val	GCG Ala	CCG Pro	CAC His	AAC Asn	GAC Asp	TCG Ser	GCC Ala	ACC Thr	GGG Gly	GAG Glu	CCC Pro	GAG Glu	GCG Ala	TCC Ser	864

003360 030300

	275						280						285						
5	TCG	GGC	TCG	GGG	CCG	CCT	TCC	GGG	GGC	GCA	CTG	GGG	CCT	CGG	GCG	CTG	912		
	Ser	Gly	Ser	Gly	Pro	Pro	Ser	Gly	Gly	Ala	Leu	Gly	Pro	Arg	Ala	Leu			
	290						295					300							
10	TTC	GCC	AGC	CGC	GTG	CGC	CCG	GGC	CAG	CGC	GTG	TAC	GTG	GTG	GCC	GAG	960		
	Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val	Ala	Glu			
	305					310					315					320			
15	CGT	GAC	GGG	GAC	CGC	CGG	CTC	CTG	CCC	GCC	GCT	GTG	CAC	AGC	GTG	ACC	1008		
	Arg	Asp	Gly	Asp	Arg	Arg	Leu	Leu	Pro	Ala	Ala	Val	His	Ser	Val	Thr			
					325					330					335				
20	CTA	AGC	GAG	GAG	GCC	GCG	GGC	GCC	TAC	GCG	CCG	CTC	ACG	GCC	CAG	GGC	1056		
	Leu	Ser	Glu	Glu	Ala	Ala	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Ala	Gln	Gly			
					340				345					350					
25	ACC	ATT	CTC	ATC	AAC	CGG	GTG	CTG	GCC	TCG	TGC	TAC	GCG	GTC	ATC	GAG	1104		
	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Ile	Glu			
			355					360					365						
30	GAG	CAC	AGC	TGG	GCG	CAC	CGG	GCC	TTC	GCG	CCC	TTC	CGC	CTG	GCG	CAC	1152		
	Glu	His	Ser	Trp	Ala	His	Arg	Ala	Phe	Ala	Pro	Phe	Arg	Leu	Ala	His			
		370					375					380							
35	GCG	CTC	CTG	GCT	GCA	CTG	GCG	CCC	GCG	CGC	ACG	GAC	CGC	GGC	GGG	GAC	1200		
	Ala	Leu	Leu	Ala	Ala	Leu	Ala	Pro	Ala	Arg	Thr	Asp	Arg	Gly	Gly	Asp			
	385					390					395					400			
40	AGC	GGC	GGC	GGG	GAC	CGC	GGG	GGC	GGC	GGC	AGA	GTA	GCC	CTA	ACC		1248		
	Ser	Gly	Gly	Gly	Asp	Arg	Gly	Gly	Gly	Gly	Gly	Arg	Val	Ala	Leu	Thr			
					405				410					415					
45	GCT	CCA	GGT	GCT	GCC	GAC	GCT	CCG	GGT	GCG	GGG	GCC	ACC	GCG	GGC	ATC	1296		
	Ala	Pro	Gly	Ala	Ala	Asp	Ala	Pro	Gly	Ala	Gly	Ala	Thr	Ala	Gly	Ile			
					420				425				430						
50	CAC	TGG	TAC	TCG	CAG	CTG	CTC	TAC	CAA	ATA	GGC	ACC	TGG	CTC	CTG	GAC	1344		
	His	Trp	Tyr	Ser	Gln	Leu	Leu	Tyr	Gln	Ile	Gly	Thr	Trp	Leu	Leu	Asp			
			435					440					445						
55	AGC	GAG	GCC	CTG	CAC	CCG	CTG	GGC	ATG	GCG	GTC	AAG	TCC	AGC	NNN	AGC	1392		
	Ser	Glu	Ala	Leu	His	Pro	Leu	Gly	Met	Ala	Val	Lys	Ser	Ser	Xaa	Ser			
		450					455				460								
60	CGG	GGG	GCC	GGG	GGA	GGG	GCG	CGG	GAG	GGG	GCC						1425		
	Arg	Gly	Ala	Gly	Gly	Gly	Ala	Arg	Glu	Gly	Ala								
	465					470					475								

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 51..1283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

5
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CATCAGCCCA CCAGGAGACC TCGCCCGCCG CTCCCCCGGG CTCCCCGGCC ATG TCT
 Met Ser
 1

CCC GCC CGG CTC CGG CCC CGA CTG CAC TTC TGC CTG GTC CTG TTG CTG
 Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu Leu Leu
 5 10 15

CTG CTG GTG GTG CCC GCG GCA TGG GGC TGC GGG CCG GGT CGG GTG GTG
 Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg Val Val
 20 25 30

GGC AGC CGC CGG CGA CCG CCA CGC AAA CTC GTG CCG CTC GCC TAC AAG
 Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala Tyr Lys
 35 40 45 50

CAG TTC AGC CCC AAT GTG CCC GAG AAG ACC CTG GGC GCC AGC GGA CGC
 Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser Gly Arg
 55 60 65

TAT GAA GGC AAG ATC GCT CGC AGC TCC GAG CGC TTC AAG GAG CTC ACC
 Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu Leu Thr
 70 75 80

CCC AAT TAC AAT CCA GAC ATC ATC TTC AAG GAC GAG GAG AAC ACA GGC
 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
 85 90 95

GCC GAC CGC CTC ATG ACC CAG CGC TGC AAG GAC CGC CTG AAC TCG CTG
 Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn Ser Leu
 100 105 110

GCT ATC TCG GTG ATG AAC CAG TGG CCC GGT GTG AAG CTG CGG GTG ACC
 Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
 115 120 125 130

GAG GGC TGG GAC GAG GAC GGC CAC CAC TCA GAG GAG TCC CTG CAT TAT
 Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
 135 140 145

GAG GGC CGC GCG GTG GAC ATC ACC ACA TCA GAC CGC GAC CGC AAT AAG
 Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys
 150 155 160

TAT GGA CTG CTG GCG CGC TTG GCA GTG GAG GCC GGC TTT GAC TGG GTG
 Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
 165 170 175

TAT TAC GAG TCA AAG GCC CAC GTG CAT TGC TCC GTC AAG TCC GAG CAC
 Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser Glu His
 632

CCDS:209522.60

	180					185						190						
5	TCG	GCC	GCA	GCC	AAG	ACG	GGC	GGC	TGC	TTC	CCT	GCC	GGA	GCC	CAG	GTA		680
	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	Gln	Val		
	195					200					205					210		
10	CGC	CTG	GAG	AGT	GGG	GCG	CGT	GTG	GCC	TTG	TCA	GCC	GTG	AGG	CCG	GGA		728
	Arg	Leu	Glu	Ser	Gly	Ala	Arg	Val	Ala	Leu	Ser	Ala	Val	Arg	Pro	Gly		
					215					220					225			
15	GAC	CGT	GTG	CTG	GCC	ATG	GGG	GAG	GAT	GGG	AGC	CCC	ACC	TTC	AGC	GAT		776
	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Ser	Pro	Thr	Phe	Ser	Asp		
				230					235					240				
20	GTG	CTC	ATT	TTC	CTG	GAC	CGC	GAG	CCC	CAC	AGG	CTG	AGA	GCC	TTC	CAG		824
	Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	His	Arg	Leu	Arg	Ala	Phe	Gln		
			245					250					255					
25	GTC	ATC	GAG	ACT	CAG	GAC	CCC	CCA	CGC	CGC	CTG	GCA	CTC	ACA	CCC	GCT		872
	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	Pro	Ala		
		260					265					270						
30	CAC	CTG	CTC	TTT	ACG	GCT	GAC	AAT	CAC	ACG	GAG	CCG	GCA	GCC	CGC	TTC		920
	His	Leu	Leu	Phe	Thr	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala	Arg	Phe		
	275					280					285					290		
35	CGG	GCC	ACA	TTT	GCC	AGC	CAC	GTG	CAG	CCT	GGC	CAG	TAC	GTG	CTG	GTG		968
	Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val	Leu	Val		
					295					300					305			
40	GCT	GGG	GTG	CCA	GGC	CTG	CAG	GCT	GCC	CGC	GTG	GCA	GCT	GTC	TCT	ACA		1016
	Ala	Gly	Val	Pro	Gly	Leu	Gln	Pro	Ala	Arg	Val	Ala	Ala	Val	Ser	Thr		
				310				315						320				
45	CAC	GTG	GCC	CTC	GGG	GCC	TAC	GCC	CCG	CTC	ACA	AAG	CAT	GGG	ACA	CTG		1064
	His	Val	Ala	Leu	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Lys	His	Gly	Thr	Leu		
			325					330					335					
50	GTG	GTG	GAG	GAT	GTG	GTG	GCA	TCC	TGC	TTC	GCG	GCC	GTG	GCT	GAC	CAC		1112
	Val	Val	Glu	Asp	Val	Val	Ala	Ser	Cys	Phe	Ala	Ala	Val	Ala	Asp	His		
		340					345					350						
55	CAC	CTG	GCT	CAG	TTG	GCC	TTC	TGG	CCC	CTG	AGA	CTC	TTT	CAC	AGC	TTG		1160
	His	Leu	Ala	Gln	Leu	Ala	Phe	Trp	Pro	Leu	Arg	Leu	Phe	His	Ser	Leu		
	355				360					365						370		
60	GCA	TGG	GGC	AGC	TGG	ACC	CCG	GGG	GAG	GGT	GTG	CAT	TGG	TAC	CCC	CAG		1208
	Ala	Trp	Gly	Ser	Trp	Thr	Pro	Gly	Glu	Gly	Val	His	Trp	T				

AAGGGACCTG AGCTGGGGGA CACTGGCTCC TGCCATCTCC TCTGCCATGA AGATACACCA 1423
TTGAGACTTG ACTGGGCAAC ACCAGCGTCC CCCACCCGCG TCGTGGTGTA GTCATAGAGC 1483
5 TGCAAGCTGA GCTGGCGAGG GGATGGTTGT TGACCCCTCT CTCCTAGAGA CCTTGAGGCT 1543
GGCACGGCGA CTCCCAACTC AGCCTGCTCT CACTACGAGT TTTCATACTC TGCCTCCCCC 1603
ATTGGGAGGG CCCATTCCC 1622

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..1191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG GCT CTC CTG ACC AAT CTA CTG GCC TTG TGC TGC TTG GCA CTT CTG 48
Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
1 5 10 15
GCG CTG CCA GCC CAG AGC TGC GGG CCG GGC CGG GGG CCG GTT GGC CGG 96
Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
20 25 30
CGC CGC TAT GCG CGC AAG CAG CTC GTG CCG CTA CTC TAC AAG CAA TTT 144
Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
35 40 45
GTG CCC GGC GTG CCA GAG CGG ACC CTG GGC GCC AGT GGG CCA GCG GAG 192
Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
50 55 60
GGG AGG GTG GCA AGG GGC TCC GAG CGC TTC CGG GAC CTC GTG CCC AAC 240
Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
65 70 75 80
TAC AAC CCC GAC ATC ATC TTC AAG GAT GAG GAG AAC AGT GGA GCC GAC 288
Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
85 90 95
CGC CTG ATG ACC GAG CGT TGC AAG GAG AGG GTG AAC GCT TTG GCC ATT 336
Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
100 105 110
GCC GTG ATG AAC ATG TGG CCC GGA GTG CGC CTA CGA GTG ACT GAG GGC 384
Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
115 120 125

[illegible]

	TGG	GAC	GAG	GAC	GGC	CAC	CAC	GCT	CAG	GAT	TCA	CTC	CAC	TAC	GAA	GGC	432
	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly	
	130						135					140					
5	CGT	GCT	TTG	GAC	ATC	ACT	ACG	TCT	GAC	CGC	GAC	CGC	AAC	AAG	TAT	GGG	480
	Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly	
	145					150					155					160	
10	TTG	CTG	GCG	CGC	CTC	GCA	GTG	GAA	GCC	GGC	TTC	GAC	TGG	GTC	TAC	TAC	528
	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
					165					170					175		
15	GAG	TCC	CGC	AAC	CAC	GTC	CAC	GTG	TGC	GTC	AAA	GCT	GAT	AAC	TCA	CTG	576
	Glu	Ser	Arg	Asn	His	Val	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu	
				180					185					190			
20	GCG	GTC	CGG	GCG	GGC	GGC	TGC	TTT	CCG	GGA	AAT	GCA	ACT	GTG	CGC	CTG	624
	Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu	
			195					200					205				
25	TGG	AGC	GGC	GAG	CGG	AAA	GGG	CTG	CGG	GAA	CTG	CAC	CGC	GGA	GAC	TGG	672
	Trp	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp	
		210					215					220					
30	GTT	TTG	GCG	GCC	GAT	GCG	TCA	GGC	CGG	GTG	GTG	CCC	ACG	CCG	GTG	CTG	720
	Val	Leu	Ala	Ala	Asp	Ala	Ser	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu	
		225				230					235					240	
35	CTC	TTC	CTG	GAC	CGG	GAC	TTG	CAG	CGC	CGG	GCT	TCA	TTT	GTG	GCT	GTG	768
	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val	
					245					250					255		
40	GAG	ACC	GAG	TGG	CCT	CCA	CGC	AAA	CTG	TTG	CTC	ACG	CCC	TGG	CAC	CTG	816
	Glu	Thr	Glu	Trp	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu	
				260					265					270			
45	GTG	TTT	GCC	GCT	CGA	GGG	CCG	GCG	CCC	GCG	CCA	GGC	GAC	TTT	GCA	CCG	864
	Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro	
			275				280						285				
50	GTG	TTC	GCG	CGC	CGG	CTA	CGC	GCT	GGG	GAC	TGC	GTG	CTG	GCG	CCC	GGC	912
	Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly	
		290				295						300					
55	GGG	GAT	GCG	CTT	CGG	CCA	GCG	CGC	GTG	GCC	CGT	GTG	GCG	CGG	GAG	GAA	960
	Gly	Asp	Ala	Leu	Arg	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu	
		305				310					315					320	
60	GCC	GTG	GGC	GTG	TTC	GCG	CCG	CTC	ACC	GCG	CAC	GGG	ACG	CTG	CTG	GTG	1

CTG	CTC	CCC	GGC	GGG	GCC	GTC	CAG	CCG	ACT	GGC	ATG	CAT	TGG	TAC	TCT	1152
Leu	Leu	Pro	Gly	Gly	Ala	Val	Gln	Pro	Thr	Gly	Met	His	Trp	Tyr	Ser	
	370					375					380					

5 CGG CTC CTC TAC CGC TTA GCG GAG GAG CTA CTG GGC TG 1191
Arg Leu Leu Tyr Arg Ileu Ala Glu Glu Leu Leu Gly
385 390 395

10 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) **FEATURE:**

- (A) NAME/KEY: CDS
(B) LOCATION: 1..1248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

30 ATG GAC GTA AGG CTG CAT CTG AAG CAA TTT GCT TTA CTG TGT TTT ATC 48
 Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile
 1 5 10 15

AGC TTG CTT CTG ACG CCT TGT GGA TTA GCC TGT GGT CCT GGT AGA GGT 96
Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly
35 20 25 30

TAT GGA AAA CGA AGA CAC CCA AAG AAA TTA ACC CCG TTG GCT TAC AAG 144
Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
35 40 45

CAA TTC ATC CCC AAC GTT GCT GAG AAA ACG CTT GGA GCC AGC GGC AAA 192
Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys
50 55 60

45 TAC GAA GGC AAA ATC ACA AGG AAT TCA GAG AGA TTT AAA GAG CTG ATT 240
Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile
65 70 75 80

50 CCG AAT TAT AAT CCC GAT ATC ATC TTT AAG GAC GAG GAA AAC ACA AAC 288
Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn
85 90 95

55 GCT GAC AGG CTG ATG ACC AAG CGC TGT AAG GAC AAG TTA AAT TCG TTG 336
Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu
100 105 110

GCC ATA TCC GTC ATG AAC CAC TGG CCC GGC GTG AAA CTG CGC GTC ACT 384
Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr
115 120 125

	GAA	GGC	TGG	GAT	GAG	GAT	GGT	CAC	CAT	TTA	GAA	GAA	TCT	TTG	CAC	TAT	432
	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Leu	Glu	Glu	Ser	Leu	His	Tyr	
	130						135					140					
5	GAG	GGA	CGG	GCA	GTG	GAC	ATC	ACT	ACC	TCA	GAC	AGG	GAT	AAA	AGC	AAG	480
	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Lys	Ser	Lys	
	145					150					155					160	
10	TAT	GGG	ATG	CTA	TCC	AGG	CTT	GCA	GTG	GAG	GCA	GGA	TTC	GAC	TGG	GTC	528
	Tyr	Gly	Met	Leu	Ser	Arg	Ile	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	
					165					170					175		
15	TAT	TAT	GAA	TCT	AAA	GCC	CAC	ATA	CAC	TGC	TCT	GTC	AAA	GCA	GAA	AAT	576
	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	
				180					185					190			
20	TCA	GTG	GCT	GCT	AAA	TCA	GGA	GGA	TGT	TTT	CCT	GGG	TCT	GGG	ACG	GTG	624
	Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Gly	Thr	Val	
			195				200						205				
25	ACA	CTT	GGT	GAT	GGG	ACG	AGG	AAA	CCC	ATC	AAA	GAT	CTT	AAA	GTG	GGC	672
	Thr	Leu	Gly	Asp	Gly	Thr	Arg	Lys	Pro	Ile	Lys	Asp	Leu	Lys	Val	Gly	
		210					215					220					
30	GAC	CGG	GTT	TTG	GCT	GCA	GAC	GAG	AAG	GGA	AAT	GTC	TTA	ATA	AGC	GAC	720
	Asp	Arg	Val	Leu	Ala	Ala	Asp	Glu	Lys	Gly	Asn	Val	Leu	Ile	Ser	Asp	
	225					230					235					240	
35	TTT	ATT	ATG	TTT	ATA	GAC	CAC	GAT	CCG	ACA	ACG	AGA	AGG	CAA	TTC	ATC	768
	Phe	Ile	Met	Phe	Ile	Asp	His	Asp	Pro	Thr	Arg	Arg	Gln	Phe	Ile		
					245				250					255			
40	GTC	ATC	GAG	ACG	TCA	GAA	CCT	TTC	ACC	AAG	CTC	ACC	CTC	ACT	GCC	GCG	816
	Val	Ile	Glu	Thr	Ser	Glu	Pro	Phe	Thr	Lys	Leu	Thr	Leu	Thr	Ala	Ala	
				260					265					270			
45	CAC	CTA	GTT	TTC	GTT	GGA	AAC	TCT	TCA	GCA	GCT	TCG	GGT	ATA	ACA	GCA	864
	His	Leu	Val	Phe	Val	Gly	Asn	Ser	Ser	Ala	Ala	Ser	Gly	Ile	Thr	Ala	
			275					280					285				
50	ACA	TTT	GCC	AGC	AAC	GTG	AAG	CCT	GGA	GAT	ACA	GTT	TTA	GTG	TGG	GAA	912
	Thr	Phe	Ala	Ser	Asn	Val	Lys	Pro	Gly	Asp	Thr	Val	Leu	Val	Trp	Glu	
		290					295					300					
55	GAC	ACA	TGC	GAG	AGC	CTC	AAG	AGC	GTT	ACA	GTG	AAA	AGG	ATT	TAC	ACT	960
	Asp	Thr	Cys	Glu	Ser	Leu	Lys	Ser	Val	Thr	Val	Lys	Arg	Ile	Tyr	Thr	
	305					310					315					320	
60	GAG	GAG	CAC	GAG	GGC	TCT	TTT	GCG	CCA	GTC	ACC	GCG	CAC	GGA	ACC	ATA	1008
	Glu	Glu	His	Glu	Gly	Ser	Phe	Ala	Pro	Val	Thr	Ala	His	Gly	Thr	Ile	
					325					330					335		
65	ATA	GTG	GAT	CAG	GTG	TTG	GCA	TCG	TGC	TAC	GCG	GTC	ATT	GAG	AAC	CAC	1056
	Ile	Val	Asp	Gln	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Ile	Glu	Asn	His	
				340					345					350			
70	AAA	TGG	GCA	CAT	TGG	GCT	TTT	GCG	CCG	GTC	AGG	TTG	TGT	CAC	AAG	CTG	1104
	Lys	Trp	Ala	His	Trp	Ala	Phe	Ala	Pro	Val	Arg	Leu	Cys	His	Lys	Leu	
			355					360					365				

003500 003500

ATG ACG TGG CTT TTT CCG GCT CGT GAA TCA AAC GTC AAT TTT CAG GAG 1152
Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu
370 375 380

5 GAT GGT ATC CAC TGG TAC TCA AAT ATG CTG TTT CAC ATC GGC TCT TGG 1200
Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp
385 390 395 400

10 CTG CTG GAC AGA GAC TCT TTC CAT CCA CTC GGG ATT TTA CAC TTA AGT 1248
Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser
405 410 415

TGA 1251

15

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 425 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
1 5 10 15

30 Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
20 25 30

35 Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
35 40 45

Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
50 55 60

40 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
65 70 75 80

Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
85 90 95

45

Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
100 105 110

50 Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
115 120 125

Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
130 135 140

55 Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys
145 150 155 160

Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
165 170 175

60

00335001003030

003550-0609

Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
 180 185 190
 5 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
 195 200 205
 His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
 210 215 220
 10 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
 225 230 235 240
 Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
 245 250 255
 15 Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala
 260 265 270
 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
 275 280 285
 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
 290 295 300
 25 Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser
 305 310 315 320
 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
 325 330 335
 30 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
 340 345 350
 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
 355 360 365
 35 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
 370 375 380
 40 Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
 385 390 395 400
 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
 405 410 415
 45 Pro Leu Gly Met Val Ala Pro Ala Ser
 420 425

50 (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55

- (ii) MOLECULE TYPE: protein

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

	Met	Ala	Leu	Pro	Ala	Ser	Leu	Leu	Pro	Leu	Cys	Cys	Leu	Ala	Leu	Leu
5	1				5					10					15	
	Ala	Leu	Ser	Ala	Gln	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Pro	Val	Gly	Arg
				20					25					30		
10	Arg	Arg	Tyr	Val	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe
			35					40					45			
	Val	Pro	Ser	Met	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu
		50					55					60				
15	Gly	Arg	Val	Thr	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn
	65					70					75					80
	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp
					85					90					95	
20	Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile
				100					105					110		
	Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly
25			115					120					125			
	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly
		130					135					140				
30	Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly
	145					150					155					160
	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr
					165					170					175	
35	Glu	Ser	Arg	Asn	His	Ile	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu
				180					185					190		
	Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu
40			195					200					205			
	Arg	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp
		210					215					220				
45	Val	Leu	Ala	Ala	Asp	Ala	Ala	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu
	225					230					235					240
	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val
					245					250					255	
50	Glu	Thr	Glu	Arg	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu
				260					265					270		
	Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro
55			275					280					285			
	Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly
							295					300				
60	Gly	Asp	Ala	Leu	Gln	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu

[illegible]

305 310 315 320
 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
 325 330 335
 5 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
 340 345 350
 10 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
 355 360 365
 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
 370 375 380
 15 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
 385 390 395

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
 1 5 10 15
 35 Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
 20 25 30
 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
 35 40 45
 40 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
 50 55 60
 45 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
 65 70 75 80
 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
 85 90 95
 50 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
 100 105 110
 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
 115 120 125
 55 Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
 130 135 140
 60 His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
 145 150 155 160

002502 060300

Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
 165 170 175
 5 Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
 180 185 190
 Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
 195 200 205
 10 Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys
 210 215 220
 Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe
 225 230 235 240
 15 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala
 245 250 255
 20 Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
 260 265 270
 Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala
 275 280 285
 25 His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val
 290 295 300
 30 Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
 305 310 315 320
 Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly
 325 330 335
 35 Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
 340 345 350
 Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro
 355 360 365
 40 Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr
 370 375 380
 45 Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Ser Thr
 385 390 395 400
 Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
 405 410

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

5 Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser
 1 5 10 15
 Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly
 20 25 30
 10 Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe
 35 40 45
 15 Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu
 50 55 60
 Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn
 65 70 75 80
 20 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp
 85 90 95
 Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile
 100 105 110
 25 Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125
 Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly
 130 135 140
 Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly
 145 150 155 160
 35 Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
 165 170 175
 Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val
 180 185 190
 40 Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu
 195 200 205
 Glu Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Arg Pro Gly Asp Arg
 210 215 220
 Val Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu
 225 230 235 240
 50 Thr Phe Leu Asp Arg Asp Glu Gly Ala Lys Lys Val Phe Tyr Val Ile
 245 250 255
 Glu Thr Leu Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu
 260 265 270
 55 Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro Gly Pro Ser
 275 280 285
 Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val
 290 295 300

003503-03099

Ala	Glu	Arg	Gly	Gly	Asp	Arg	Arg	Leu	Leu	Pro	Ala	Ala	Val	His	Ser
305					310					315					320
Val	Thr	Leu	Arg	Glu	Glu	Glu	Ala	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Ala
				325					330					335	
His	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val
			340					345					350		
Ile	Glu	Glu	His	Ser	Trp	Ala	His	Arg	Ala	Phe	Ala	Pro	Phe	Arg	Leu
			355				360					365			
Ala	His	Ala	Leu	Leu	Ala	Ala	Leu	Ala	Pro	Ala	Arg	Thr	Asp	Gly	Gly
	370					375					380				
Gly	Gly	Gly	Ser	Ile	Pro	Ala	Ala	Gln	Ser	Ala	Thr	Glu	Ala	Arg	Gly
385					390					395					400
Ala	Glu	Pro	Thr	Ala	Gly	Ile	His	Trp	Tyr	Ser	Gln	Leu	Leu	Tyr	His
				405					410					415	
Ile	Gly	Thr	Trp	Leu	Leu	Asp	Ser	Glu	Thr	Met	His	Pro	Leu	Gly	Met
			420					425					430		
Ala	Val	Lys	Ser	Ser											
			435												
(2) INFORMATION FOR SEQ ID NO:14:															
(i) SEQUENCE CHARACTERISTICS:															
(A) LENGTH: 418 amino acids															
(B) TYPE: amino acid															
(D) TOPOLOGY: linear															
(ii) MOLECULE TYPE: protein															
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:															
Met	Arg	Leu	Leu	Thr	Arg	Val	Leu	Leu	Val	Ser	Leu	Leu	Thr	Leu	Ser
1				5					10					15	
Leu	Val	Val	Ser	Gly	Leu	Ala	Cys	Gly	Pro	Gly	Arg	Gly	Tyr	Gly	Arg
			20					25					30		
Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile
		35					40					45			
Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly
	50					55					60				
Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr
65					70					75					80
Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg
				85					90						95

	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ser	Leu	Ala	Ile	Ser
				100					105					110		
5	Val	Met	Asn	His	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	Glu	Gly	Trp
			115					120					125			
	Asp	Glu	Asp	Gly	His	His	Phe	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg
		130					135					140				
10	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Lys	Ser	Lys	Tyr	Gly	Thr
		145				150					155					160
	Leu	Ser	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu
				165						170					175	
15	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala
				180					185				190			
20	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Leu	Val	Ser	Leu	Gln
			195					200					205			
	Asp	Gly	Gly	Gln	Lys	Ala	Val	Lys	Asp	Leu	Asn	Pro	Gly	Asp	Lys	Val
		210					215					220				
25	Leu	Ala	Ala	Asp	Ser	Ala	Gly	Asn	Leu	Val	Phe	Ser	Asp	Phe	Ile	Met
		225				230					235					240
	Phe	Thr	Asp	Arg	Asp	Ser	Thr	Thr	Arg	Arg	Val	Phe	Tyr	Val	Ile	Glu
				245					250						255	
30	Thr	Gln	Glu	Pro	Val	Glu	Lys	Ile	Thr	Leu	Thr	Ala	Ala	His	Leu	Leu
			260						265					270		
	Phe	Val	Leu	Asp	Asn	Ser	Thr	Glu	Asp	Leu	His	Thr	Met	Thr	Ala	Ala
35			275					280					285			
	Tyr	Ala	Ser	Ser	Val	Arg	Ala	Gly	Gln	Lys	Val	Met	Val	Val	Asp	Asp
		290					295					300				
40	Ser	Gly	Gln	Leu	Lys	Ser	Val	Ile	Val	Gln	Arg	Ile	Tyr	Thr	Glu	Glu
		305				310					315					320
	Gln	Arg	Gly	Ser	Phe	Ala	Pro	Val	Thr	Ala	His	Gly	Thr	Ile	Val	Val
				325						330					335	
45	Asp	Arg	Ile	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Ile	Glu	Asp	Gln	Gly	Leu
			340						345					350		
	Ala	His	Leu	Ala	Phe	Ala	Pro	Ala	Arg	Leu	Tyr	Tyr	Tyr	Val	Ser	Ser
50			355					360					365			
	Phe	Leu	Ser	Pro	Lys	Thr	Pro	Ala	Val	Gly	Pro	Met	Arg	Leu	Tyr	Asn
		370					375					380				
55	Arg	Arg	Gly	Ser	Thr	Gly	Thr	Pro	Gly	Ser	Cys	His	Gln	Met	Gly	Thr
		385				390					395					400
	Trp	Leu	Leu	Asp	Ser	Asn	Met	Leu	His	Pro	Leu	Gly	Met	Ser	Val	Asn
				405						410					415	
60																

5 (2) INFORMATION FOR SEQ ID NO:15:

(A) LENGTH: 475 amino acids

(D) TOPOLOGY: linear

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys
20 25 30

Arg Arg His Pro Lys Lys Leu Thr / Pro Leu Ala Tyr Lys Gln Phe Ile
35 40 45

Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
50 55 60

Lys Ile Ser Arg Asn Ser Glu Arg Phe / Lys Glu Leu Thr Pro Asn Tyr
65 70 75 80

Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
85 90 95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser
100 105 110

Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
115 120 125

Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg
130 135 140

Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met
145 150 155 160

Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
165 170 175

Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu ~~Asn~~ Ser Val Ala
180 185 190

Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val / His Leu Glu
195 200 205

Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val
210 215 220

Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Ser Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu
1 5 10 15

Leu Leu Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg
 20 25 30
 5 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
 35 40 45
 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
 50 55 60
 10 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
 65 70 75 80
 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
 85 90 95
 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
 100 105 110
 20 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
 115 120 125
 Val Thr Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
 130 135 140
 25 His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
 145 150 155 160
 Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
 165 170 175
 Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
 180 185 190
 35 Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
 195 200 205
 Gln Val Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg
 210 215 220
 40 Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe
 225 230 235 240
 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala
 245 250 255
 Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
 260 265 270
 50 Pro Ala His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala
 275 280 285
 Arg Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val
 290 295 300
 55 Leu Val Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
 305 310 315 320
 Ser Thr His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly
 325 330 335

003360 0609
 000000 209500

1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405</
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-118-

Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu
180 185 190

Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
195 200 205

Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
210 215 220

Val	Leu	Ala	Ala	Asp	Ala	Ser	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu
225					230					235					240

Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
245 250 255

Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
260 265 270

Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
275 280 285

Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
290 295 300

Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
305 310 315 320

Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
325 330 335

Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
340 345 350

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
355 360 365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
370 375 380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly
385 390 395

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 416 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu ~~Leu~~ Cys Phe Ile
1 5 10 15

Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly
20 25 30

66E090"20352260

	Tyr	Gly	Lys	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	
			35					40					45				
5	Gln	Phe	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Lys	
		50					55					60					
	Tyr	Glu	Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Ile	
	65					70					75					80	
10	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Asn	
				85						90					95		
	Ala	Asp	Arg	Leu	Met	Thr	Lys	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ser	Leu	
15				100					105					110			
	Ala	Ile	Ser	Val	Met	Asn	His	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	
			115					120					125				
20	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Leu	Glu	Glu	Ser	Leu	His	Tyr	
		130					135					140					
	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Lys	Ser	Lys	
	145					150					155					160	
25	Tyr	Gly	Met	Leu	Ser	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	
				165						170					175		
	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	
30				180					185					190			
	Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Gly	Thr	Val	
		195						200					205				
35	Thr	Leu	Gly	Asp	Gly	Thr	Arg	Lys	Pro	Ile	Lys	Asp	Leu	Lys	Val	Gly	
		210					215					220					
	Asp	Arg	Val	Leu	Ala	Ala	Asp	Glu	Lys	Gly	Asn	Val	Leu	Ile	Ser	Asp	
	225					230					235					240	
40	Phe	Ile	Met	Phe	Ile	Asp	His	Asp	Pro	Thr	Thr	Arg	Arg	Gln	Phe	Ile	
				245						250					255		
	Val	Ile	Glu	Thr	Ser	Glu	Pro	Phe	Thr	Lys	Leu	Thr	Leu	Thr	Ala	Ala	
45				260						265					270		
	His	Leu	Val	Phe	Val	Gly	Asn	Ser	Ser	Ala	Ala	Ser	Gly	Ile	Thr	Ala	
			275				280						285				
50	Thr	Phe	Ala	Ser	Asn	Val	Lys	Pro	Gly	Asp	Thr	Val	Leu	Val	Trp	Glu	
		290					295					300					
	Asp	Thr	Cys	Glu	Ser	Leu	Lys	Ser	Val	Thr	Val	Lys	Arg	Ile	Tyr	Thr	
	305					310					315				320		
55	Glu	Glu	His	Glu	Gly	Ser	Phe	Ala	Pro	Val	Thr	Ala	His	Gly	Thr	Ile	
				325						330					335		
	Ile	Val	Asp	Gln	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Ile	Glu	Asn	His	
60				340					345					350			

[illegible]

	GAG	TAC	ACG	AAC	AGC	GCC	TCC	GGA	CCT	CTG	GAG	GGT	GTG	ATC	CGT	CGG	384
	Glu	Tyr	Thr	Asn	Ser	Ala	Ser	Gly	Pro	Leu	Glu	Gly	Val	Ile	Arg	Arg	
			115					120					125				
5	GAT	TCG	CCC	AAA	TTC	AAG	GAC	CTC	GTG	CCC	AAC	TAC	AAC	AGG	GAC	ATC	432
	Asp	Ser	Pro	Lys	Phe	Lys	Asp	Leu	Val	Pro	Asn	Tyr	Asn	Arg	Asp	Ile	
		130					135					140					
10	CTT	TTC	CGT	GAC	GAG	GAA	GGC	ACC	GGA	GCG	GAT	GGC	TTG	ATG	AGC	AAG	480
	Leu	Phe	Arg	Asp	Glu	Glu	Gly	Thr	Gly	Ala	Asp	Gly	Leu	Met	Ser	Lys	
		145				150					155					160	
15	CGC	TGC	AAG	GAG	AAG	CTA	AAC	GTG	CTG	GCC	TAC	TCG	GTG	ATG	AAC	GAA	528
	Arg	Cys	Lys	Glu	Lys	Leu	Asn	Val	Leu	Ala	Tyr	Ser	Val	Met	Asn	Glu	
					165					170					175		
20	TGG	CCC	GGC	ATC	CGG	CTG	CTG	GTC	ACC	GAG	AGC	TGG	GAC	GAG	GAC	TAC	576
	Trp	Pro	Gly	Ile	Arg	Leu	Leu	Val	Thr	Glu	Ser	Trp	Asp	Glu	Asp	Tyr	
				180					185					190			
25	CAT	CAC	GGC	CAG	GAG	TCG	CTC	CAC	TAC	GAG	GGC	CGA	GCG	GTG	ACC	ATT	624
	His	His	Gly	Gln	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Val	Thr	Ile	
			195				200						205				
30	GCC	ACC	TCC	GAT	CGC	GAC	CAG	TCC	AAA	TAC	GGC	ATG	CTC	GCT	CGC	CTG	672
	Ala	Thr	Ser	Asp	Arg	Asp	Gln	Ser	Lys	Tyr	Gly	Met	Leu	Ala	Arg	Leu	
		210					215				220						
35	GCC	GTC	GAG	GCT	GGA	TTC	GAT	TGG	GTC	TCC	TAC	GTC	AGC	AGG	CGC	CAC	720
	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Ser	Tyr	Val	Ser	Arg	Arg	His	
		225				230					235					240	
40	ATC	TAC	TGC	TCC	GTC	AAG	TCA	GAT	TCG	TCG	ATC	AGT	TCC	CAC	GTG	CAC	768
	Ile	Tyr	Cys	Ser	Val	Lys	Ser	Asp	Ser	Ser	Ile	Ser	Ser	His	Val	His	
				245					250					255			
45	GGC	TGC	TTC	ACG	CCG	GAG	AGC	ACA	GCG	CTG	CTG	GAG	AGT	GGA	GTC	CGG	816
	Gly	Cys	Phe	Thr	Pro	Glu	Ser	Thr	Ala	Leu	Leu	Glu	Ser	Gly	Val	Arg	
				260					265					270			
50	AAG	CCG	CTC	GGC	GAG	CTC	TCT	ATC	GGA	GAT	CGT	GTT	TTG	AGC	ATG	ACC	864
	Lys	Pro	Leu	Gly	Glu	Leu	Ser	Ile	Gly	Asp	Arg	Val	Leu	Ser	Met	Thr	
			275				280						285				
55	GCC	AAC	GGA	CAG	GCC	GTC	TAC	AGC	GAA	GTG	ATC	CTC	TTC	ATG	GAC	CGC	912
	Ala	Asn	Gly	Gln	Ala	Val	Tyr	Ser	Glu	Val	Ile	Leu	Phe	Met	Asp	Arg	
		290					295					300					
60	AAC	CTC	GAG	CAG	ATG	CAA	AAC	TTT	GTG	CAG	CTG	CAC	ACG	GAC	GGT	GGA	960
	Asn	Leu	Glu	Gln	Met	Gln	Asn	Phe	Val	Gln	Leu	His	Thr	Asp	Gly	Gly	
		305				310				315						320	
65	GCA	GTG	CTC	ACG	GTG	ACG	CCG	GCT	CAC	CTG	GTT	AGC	GTT	TGG	CAG	CCG	1008
	Ala	Val	Leu	Thr	Val	Thr	Pro	Ala	His	Leu	Val	Ser	Val	Trp	Gln	Pro	
				325					330						335		
70	GAG	AGC	CAG	AAG	CTC	ACG	TTT	GTG	TTT	GCG	CAT	CGC	ATC	GAG	GAG	AAG	1056
	Glu	Ser	Gln	Lys	Leu	Thr	Phe	Val	Phe	Ala	His	Arg	Ile	Glu	Glu	Lys	
				340				345						350			

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AAC CAG GTG CTC GTA CGG GAT GTG GAG ACG GGC GAG CTG AGG CCC CAG 1104
Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln
355 360 365

5 CGA GTG GTC AAG TTG GGC AGT GTG CGC AGT AAG GGC GTG GTC GCG CCG 1152
Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro
370 375 380

10 CTG ACC CGC GAG GGC ACC ATT GTG GTC AAC TCG GTG GCC GCC AGT TGC 1200
Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys
385 390 395 400

15 TAT GCG GTG ATC AAC AGT CAG TCG CTG GCC CAC TGG GGA CTG GCT CCC 1248
Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro
405 410 415

20 ATG CGC CTG CTG TCC ACG CTG GAG GCG TGG CTG CCC GCC AAG GAG CAG 1296
Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln
420 425 430

25 TTG CAC AGT TCG CCG AAG GTG GTG AGC TCG GCG CAG CAG CAG AAT GGC 1344
Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly
435 440 445

30 ATC CAT TGG TAT GCC AAT GCG CTC TAC AAG GTC AAG GAC TAC GTG CTG 1392
Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu
450 455 460

35 CCG CAG AGC TGG CGC CAC GAT TGA 1416
Pro Gln Ser Trp Arg His Asp
465 470

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 471 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

45 Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr
1 5 10 15

Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln
20 25 30

50 Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr
35 40 45

55 Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu
50 55 60

Thr Ser Leu Val Ala Leu Leu Leu Ile Val Leu Pro Met Val Phe Ser
65 70 75 80

60 Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala

"000000" 000000

95

5	Arg	Asn	Leu	Tyr	Pro	Leu	Val	Leu	Lys	Gln	Thr	Ile	Pro	Asn	Leu	Ser
									105						110	
	Glu	Tyr	Thr	Asn	Ser	Ala	Ser	Gly	Pro	Leu	Glu	Gly	Val	Ile	Arg	Arg
			115					120					125			
10	Asp	Ser	Pro	Lys	Phe	Lys	Asp	Leu	Val	Pro	Asn	Tyr	Asn	Arg	Asp	Ile
		130					135					140				
	Leu	Phe	Arg	Asp	Glu	Glu	Gly	Thr	Gly	Ala	Asp	Gly	Leu	Met	Ser	Lys
		145				150					155					160
15	Arg	Cys	Lys	Glu	Lys	Leu	Asn	Val	Leu	Ala	Tyr	Ser	Val	Met	Asn	Glu
					165					170					175	
	Trp	Pro	Gly	Ile	Arg	Leu	Leu	Val	Thr	Glu	Ser	Trp	Asp	Glu	Asp	Tyr
				180					185					190		
20	His	His	Gly	Gln	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Val	Thr	Ile
			195					200					205			
	Ala	Thr	Ser	Asp	Arg	Asp	Gln	Ser	Lys	Tyr	Gly	Met	Leu	Ala	Arg	Leu
		210					215					220				
25	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Ser	Tyr	Val	Ser	Arg	Arg	His
		225				230					235					240
30	Ile	Tyr	Cys	Ser	Val	Lys	Ser	Asp	Ser	Ser	Ile	Ser	Ser	His	Val	His
					245					250					255	
	Gly	Cys	Phe	Thr	Pro	Glu	Ser	Thr	Ala	Leu	Leu	Glu	Ser	Gly	Val	Arg
				260					265					270		
35	Lys	Pro	Leu	Gly	Glu	Leu	Ser	Ile	Gly	Asp	Arg	Val	Leu	Ser	Met	Thr
			275					280					285			
40	Ala	Asn	Gly	Gln	Ala	Val	Tyr	Ser	Glu	Val	Ile	Leu	Phe	Met	Asp	Arg
		290					295					300				
	Asn	Leu	Glu	Gln	Met	Gln	Asn	Phe	Val	Gln	Leu	His	Thr	Asp	Gly	Gly
		305				310					315					320
45	Ala	Val	Leu	Thr	Val	Thr	Pro	Ala	His	Leu	Val	Ser	Val	Trp	Gln	Pro
					325					330					335	
	Glu	Ser	Gln	Lys	Leu	Thr	Phe	Val	Phe	Ala	His	Arg	Ile	Glu	Glu	Lys
				340					345					350		
50	Asn	Gln	Val	Leu	Val	Arg	Asp	Val	Glu	Thr	Gly	Glu	Leu	Arg	Pro	Gln
			355					360					365			
	Arg	Val	Val	Lys	Leu	Gly	Ser	Val	Arg	Ser	Lys	Gly	Val			

405 410 415

Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln
420 425 430

5 Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly
435 440 445

10 Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu
450 455 460

Pro Gln Ser Trp Arg His Asp
465 470

15 (2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

30 Cys Gly Pro Gly Arg Gly Xaa Gly Xaa Arg Arg His Pro Lys Lys Leu
1 5 10 15

Thr Pro Leu Ala Tyr Lys Gln Phe Ile Pro Asn Val Ala Glu Lys Thr
20 25 30

35 Leu Gly Ala Ser Gly Arg Tyr Glu Gly Lys Ile Xaa Arg Asn Ser Glu
35 40 45

40 Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys
50 55 60

Asp Glu Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys
65 70 75 80

45 Asp Lys Leu Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp Pro Gly
85 90 95

50 Val Xaa Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His His Xaa
100 105 110

Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser
115 120 125

55 Asp Arg Asp Xaa Ser Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala Val Glu
130 135 140

Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Ile His Cys
145 150 155 160

60 Ser Val Lys Ala Glu Asn Ser Val Ala Ala Lys Ser Gly Gly Cys Phe

00255260 00255260 00255260

165 170 175

Pro Gly Ser Ala Xaa Val Xaa Leu Xaa Xaa Gly Gly Xaa Lys Xaa Val
180 185 190

5 Lys Asp Leu Xaa Pro Gly Asp Xaa Val Leu Ala Ala Asp Xaa Xaa Gly
195 200 205

10 Xaa Leu Xaa Xaa Ser Asp Phe Xaa Xaa Phe Xaa Asp Arg
210 215 220

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg Arg Xaa Xaa Xaa Pro Lys
1 5 10 15

Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe Xaa Pro Xaa Xaa Xaa Glu
20 25 30

Xaa Thr Leu Gly Ala Ser Gly Xaa Xaa Glu Gly Xaa Xaa Xaa Arg Xaa
35 40 45

Ser Glu Arg Phe Xaa Xaa Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile
50 55 60

Phe Lys Asp Glu Glu Asn Xaa Gly Ala Asp Arg Leu Met Thr Xaa Arg
65 70 75 80

Cys Lys Xaa Xaa Xaa Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp
85 90 95

Pro Gly Val Xaa Leu Arg Val Thr Glu Gly Xaa Asp Glu Asp Gly His
100 105 110

His Xaa Xaa Xaa Ser Leu His Tyr Glu Gly Arg Ala Xaa Asp Ile Thr
115 120 125

Thr Ser Asp Arg Asp Xaa Xaa Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala
130 135 140

Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Xaa Xaa His Xaa
145 150 155 160

His Xaa Ser Val Lys Xaa Xaa
165

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